

# Power laws of complex systems from Extreme physical information

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(Dated;; Received text; Revised text; Accepted text; Published text)

## Abstract

Many complex systems obey allometric, or power, laws  $y = Yx^a$ . Here  $y \geq 0$  is the measured value of some system attribute  $a$ ,  $Y \geq 0$  is a constant, and  $x$  is a stochastic variable. Remarkably, for many living systems the exponent  $a$  is limited to values  $n/4$ ,  $n = 0, \pm 1, \pm 2, \dots$ . Here  $x$  is the mass of a randomly selected creature in the population. These quarter-power laws hold for many attributes, such as pulse rate ( $n = -1$ ). Allometry has, in the past, been theoretically justified on a case-by-case basis. An ultimate goal is to find a common cause for allometry of all types and for both living and nonliving systems. The principle  $I - J = \text{extrem. of Extreme physical information}$  (EPI) is found to provide such a cause. It describes the flow of Fisher information  $J \rightarrow I$  from an attribute value  $a$  on the cell level to its exterior observation  $y$ . Data  $y$  are formed via a system channel function  $y \equiv f(x, a)$ , with  $f(x, a)$  to be found. Extremizing the difference  $I - J$  through variation of  $f(x, a)$  results in a general allometric law  $f(x, a) \equiv y = Yx^a$ . Darwinian evolution is presumed to cause a second extremization of  $I - J$ , now with respect to the choice of  $a$ . The solution is  $a = n/4$ ,  $n = 0, \pm 1, \pm 2, \dots$ , defining the particular powers of biological allometry. Under special circumstances, the model predicts that such biological systems are controlled by but two distinct intracellular information sources. These sources are conjectured to be cellular DNA and cellular transmembrane ion gradients

## I. FISHER INFORMATION

Fisher information  $I$  is defined by the following problem of estimation. An unknown attribute value  $a$  of a system is measured as a data value  $y$ . The system's likelihood law  $p(y|a)$  is known. How well can  $a$  be estimated on the basis of  $y$ ? Assume that the estimate is to be unbiased. Then *the minimum possible mean-squared error of any such estimate is  $1/I$*  [1],[2], where

$$I \equiv I(a) \equiv \left\langle \left[ \frac{\partial}{\partial a} \ln p(y|a) \right]^2 \right\rangle_y, \quad I \geq 0. \quad (1a)$$

The notation  $\langle \dots \rangle_y$  means the expectation over all possible data values  $y$  (see also Eq. (6)). As indicated,  $I$  is positive by construction, and the dependence upon the datum  $y$  is averaged out, leaving only a dependence  $I(a)$  upon the attribute value  $a$ . Thus the information depends upon all possible  $y$ , and is a system property. Also note the reasonable tendencies: As the information becomes larger the minimum error  $1/I$  becomes smaller; etc. In its multidimensional form [3],[4],  $I$  measures system complexity as well (Sec. IV).

Information  $I(a)$  is that in *the data*. This is to be distinguished from a second type of Fisher information, denoted as  $J(a)$ , which is the amount that originates at *the source* of the data. Thus, any observation results from a flow

$$J(a) \rightarrow I(a) \quad (1b)$$

of information from source to data. This flow of information is the basis for the EPI variational approach (2) discussed further below.

Knowledge of the likelihood law  $p(y|a)$  allows  $I$  [by Eq. (1a)] and hence the minimum possible error, to be known. This minimum error can be compared, as a benchmark, with that expected from any proposed estimation approach. *This has been the traditional use of information  $I$  since about 1922* [1],[2].

However, the information  $I(a)$  is currently being used in a different way – to determine the scientific law that is obeyed by a complex system. The law defines the system through the probability density functions (PDFs)  $p(y|a)$  or probability amplitudes that characterize the system. The system is of a general nature (physical, biological, economic, etc.). For this purpose Fisher informations  $I(a)$ ,  $J(a)$  are used in the principle of "Extreme physical information" or EPI. This is a variational principle (Sec. II) whose output is the sought

law that governs the system [3],[4]. An example is the Schrodinger wave equation governing the probability amplitudes of a quantum-level system.

## II. SYSTEM AS INFORMATION CHANNEL

Consider a system consisting of a source effect specified by an attribute value  $a$ , an instrument for observing it (via probe particles), and the output space consisting of a datum  $y$  from the instrument. This defines an "information channel". Such a system is defined by its likelihood law  $p(y|a)$  and any relations among its variables  $y, a$ . The general aim of EPI is to determine the likelihood law and these relations. To facilitate finding these, the observing instrument is assumed to be ideal and noise-free.

In general, information is lost in transition from source level  $J$  to data level  $I$ . However, data tend to at least approximate their ideal (system) values, so that the loss of information tends to be minimal. Indeed, otherwise the act of observation would be pointless. Hence the principle

$$I - J = \text{extremum}, \text{ where } I \equiv I(a), J \equiv J(a), \quad J \geq 0, I = \kappa J, \quad (2)$$

$$\kappa = \kappa(a) = \text{const.}, \quad 0 \leq \kappa \leq 1.$$

This is called the principle of Extreme physical information (EPI). By (2),  $\kappa(a) \equiv I(a)/J(a)$  is a function of  $a$  and is assumed to be constant. For further details on origins of the EPI principle, see the article [3] or the books [4].

## III. ALLOMETRIC SCALING LAWS

*Note:* We use the terminology "allometry", "allometric scaling laws", "scaling laws" and "power laws" interchangeably for Eqs. (3a,b).

### A. General allometric laws

Allometric power laws have a general form

$$\mathbf{y}_n = \mathbf{Y}_n x^{a_n}, \quad a_n = \text{const.}, \quad n = 0, \pm 1, \pm 2, \dots, \pm N, \quad \mathbf{y}_n, \mathbf{Y}_n \geq 0, \quad 0 < x < \infty. \quad (3a)$$

These are simple power laws, where each member of an attribute class  $n$  obeys the same power law. The laws describe, to a good approximation, certain living and nonliving

systems. In general  $n$  defines an  $n$ th class of observed attributes  $\mathbf{y}_n \equiv y_{n1}, y_{n2}, \dots, y_{nK_n}$  of a system. Also,  $\mathbf{Y}_n \equiv Y_{n1}, Y_{n2}, \dots, Y_{nK_n}$  is a corresponding vector of *constants*, and  $K_n$  is the number of attributes in the class. Thus there is a total of  $K \equiv \sum_n K_n$  attributes over all classes. Quantity  $x$  is an *independent variable* of a system that is sampled for one of these attributes. The powers  $a_n$  in (3a) are empirically-defined values of the various attributes and are regarded as ideal identifiers of these. The  $a_n$  are generally dimensionless numbers such as  $2/3$ ,  $0.7$ , etc. Current approaches for explaining general allometry are "self organized criticality" (SOC) [5], Lande's model [6], the scale-free (SF) network property [7], and others [5].

## B. Biological allometric laws

Likewise there are many *living* systems that obey allometry [8]-[17],

$$\begin{aligned} y_{nk} &= Y_{nk} x^{a_n}, \quad a_n = n/4, \quad n = 0, \pm 1, \pm 2, \dots, \pm N, \\ k &= 1, 2, \dots, K_n, \quad y_{nk}, Y_{nk} \geq 0. \end{aligned} \tag{3b}$$

Here  $x$  is specifically the mass of the organism and the dimensionless powers  $a_n$  identify attributes of the organism. Remarkably, *each power is always some integer multiple of  $1/4$* . Why this should generally be so, both within individuals and across different species, is a great mystery of biology [9], and is addressed by this paper. Living systems have "extraordinary" complexity, and in fact are reputed to be "the most complex and diverse physical system[s] in the universe" [9]. This suggests that EPI – which applies to complex systems – is applicable to derivation of these allometric laws.

Note that the same power  $n/4$  describes all  $K_n$  members of an  $n$ th class of attributes. For example, the class  $n = -1$  has currently  $K_{-1} = 2$  known attributes, consisting of the observed heart rate and observed RNA concentration of the organism. The dynamic range of mass values  $x$  in (3b) by definition includes mass values that extend from some (unknown) *very small* and finite value to some (unknown) *very large* and finite value. Indeed, for the attribute  $n = 3$  of metabolic rate, the dynamic range of  $x$  over which (3b) is known to hold currently exceeds 27 orders of magnitude [8],[9].

Allometric laws (3b) describe both *individual* and *collective* properties of animals. Some examples are as follows. The attribute class  $n = -1$  mentioned above obeys a power  $a_{-1} = -1/4$ . The class  $n = 3$  has  $K_3 = 1$  member defining metabolic rate and obeys a

power  $a_3 = 3/4$ . Eq. (3b) even holds for a class  $n = 0$ , i.e. where the attributes do not vary with mass. An example is hemoglobin concentration in the blood, which does not vary appreciably with body (or mass) size. Other examples [9] are "metabolic rate, life span, growth rate, heart rate, DNA nucleotide substitution rate, lengths of aortas and genomes, tree height, mass of cerebral gray matter, density of mitochondria, and concentration of RNA." This list of  $K = 11$  attributes only scratches the surface.

### C. On models for biological allometry

Although many biological attributes obey the quarter-power law (3a,b), many *do not* (e.g., attributes that are the square roots of attributes that do). Nevertheless, many models exist for explaining cases of biological allometry [6],[8],[9]-[13], as conveniently summarized in [9].

However [9], these models are lacking in not providing a *unified approach* to calculating the attributes. Instead, they were "designed almost exclusively to understand only the scaling of mammalian metabolic rates, and and do not address the extraordinarily diverse, interconnected, integrated body of scaling phenomena across different species and within individuals ... Is all life organized by a few *fundamental principles*?"

A general approach would also have to predict circumstances where allometry will *not* occur. A step in this direction is to find a model that establishes necessity for *allometry of all types*, biological and nonliving. That is, it would show that:

$$\textit{If a given attribute obeys the model, then it must obey allometry.} \quad (3c)$$

We next form such a model. This dovetails with the use of EPI, which likewise requires a model.

## IV. PRIOR KNOWLEDGE

The high degree of *complexity* in allometric systems encourages us to attempt deriving the laws (3a) and (3b) by the use of EPI. Indeed EPI has been successfully used in a wide range of amplitude-estimation problems [3],[4], [18]-[25] for complex systems. Its success probably traces to its basis in Fisher information (1), which is both a measure of complexity [26], [27] and has other important physical properties [28], [29].

All uses of the EPI principle require prior knowledge of one or more invariances. Their general aim is to define the information functional  $J(a)$ . In this problem the aim is to form

a  $J(a)$  that somehow represents the *full range* of biological and physical attributes  $a \equiv a_n$  that obey laws (3a,b). *What can such a broad range of effects have in common?* One property is that of originating on the microlevel of biological cells or unit cells. Another is asymptotic behavior near the origin. The following summarizes these properties:

(i) For all systems, information  $J(a)$  originates on the *discrete microlevel*. For example, in nonliving systems such as regular crystals or irregular polymer chains, the sources are the unit cells or individual molecules, respectively. Likewise, in a living system, biological cells are the ultimate sources of information about a biological attribute  $a$ .

The information  $J(a)$  is assumed to propagate as a superposition of plane waves, from a subset of cells and cell groupings to the observer. These waves originate at a "unit cell"  $\Delta a = 1$  of  $a$ -space. (See alternative (v) below.) The discrete nature of the "cell sources" will be essential to the calculation. See Secs VII A,B. The model will also make some useful predictions on biological *sources* of the information (Sec. XII).

(ii) The allometric laws obey certain *asymptotic behaviors* near the origin, as expressed next.

Differentiating either allometric law (3a) or (3b) shows that any one allometric law (suppressing indices  $n, k$ ) obeys

$$\frac{dy}{dx} \rightarrow \infty \text{ as } x \rightarrow 0, \text{ for } a < 1, \text{ but} \quad (4a)$$

$$\frac{dy}{dx} \rightarrow 0 \text{ as } x \rightarrow 0, \text{ for } a > 1. \quad (4b)$$

In words, the rates of increase of certain attributes increase without limit, while others decrease without limit, as organism size  $x$  approaches zero. Since the size can never equal zero (as mentioned above) the trends are mathematically well defined. They also are intuitively reasonable in many cases. Hence we make these general requirement of our solution as well. Properties (4a,b) are used in Secs. IX A and E.

(iii) In *general* cases (3a) of allometry: the powers  $a_n$  are regarded as *a priori fixed numbers* of unknown size (the view taken by classical estimation theory [1]). These do not generally extremize (2). This property is used in Sec. IX E.

However, in specifically *biological* cases (3b) the  $a_n$  are presumed to be *optimal* in extremizing principle (2). That is, Darwinian evolution forces a progressive drift of organismal

attributes toward those values which confer maximal fitness on the organism. This model property is used in Secs. VIII C and IX E. Maximal fitness is taken to be achieved by those attribute values  $a$  that extremize principle (2) (see Sec. XII).

(iv) (Only) in biological cases (3b), the independent variable  $x$  is the mass of the organism. That is, laws (3b) are scaling laws covering a range of sizes, where the sizes are specified by mass values  $x$ . Why specifically "mass," is discussed in Sec. XII. In nonliving systems the nature of  $x$  depends upon the system.

(v) (Only) in biological cases (3b). Alternative to the unit-cell assumption (i) of  $\Delta a = 1$ , more generally allow  $\Delta a = L$ , some unknown constant.  $L$  should be fixed by some reasonable biological requirement. For example, the identification of the  $a_n$  with pure *numbers* requires that one be fixed as a boundary condition. Then let  $a_1 \equiv 1/4$ . In Sec. X it is found that on this basis  $L = 1$  as before.

Note that these model assumptions are not in themselves sufficient to imply the allometric laws. For example, laws (3a,b) with  $x$  incorrectly replaced by  $\sin(x)$  would still satisfy requirements (4a,b) of (ii).

Finally, not all systems obey allometry Eqs. (3a,b). Therefore, such systems do not obey this model, by the necessity condition (3c) above. This is further discussed in Sec. XII.

## V. MEASUREMENT CHANNEL FOR PROBLEM

The EPI principle will be applied to both living and nonliving systems. Thus, the measurement channel described next is, in general, that of either a living or a nonliving system. However, for definiteness, biological terminology is often used.

### A. Measurement, system function

In general, the measured value  $y$  of an attribute  $a$  is a function

$$y = Cf(x, a), \quad -\infty \leq a \leq +\infty, \quad (5)$$

for some constant  $C$  and some deterministic function  $f$ . The latter is called the "system" or "channel" function. The channel function defines how an attribute value  $y$  results from a corresponding class of attribute value  $a$  and a random source effect  $x$  within the system. Here  $x$  is a random value of the mass of a randomly chosen system (a biological creature

or a nonliving system such as a polymer). The source variable  $x$  obeys some unknown and arbitrary probability law  $p_X(x)$ . Its details will not matter to the calculation.

The overall aim of this use of EPI will be to find the constants  $C$  and the channel functions  $f(x, a)$  in the presence of any fixed but arbitrary PDF  $p_X(x)$  for the mass  $x$ . Hence, the functions  $f(x, a)$  will be varied to achieve the extremum that is required in Eq. (2). The system function will turn out to be the allometric law (3a,b). In biological cases the attribute value  $a$  will be further varied to extremize  $I - J$  in Eq. (2). The solution will equal  $n/4$ , for values of  $n = 0, \pm 1, \pm 2, \dots$

The particular *form* of the system function  $f$  defines the physics of the particular channel. As a simplistic example, for some channels not considered here,  $f(x, a) = a + x$ . This would be the familiar case of additive noise corrupting a signal value.

### B. Some caveats to EPI derivation

It should be noted that past use of EPI has been through variation of the system *PDFs* or *amplitude functions*, not through variation of their system function  $f(x, a)$  as proposed here. The success of the approach in a wide range of amplitude-estimation problems [3],[4], [18]-[22], [23], [24], [25] implies that systems in general *obey EPI through variation of their PDFs or amplitude functions*. However, it is not known at this point whether systems as well *obey EPI through variation of their channel functions*. The derivation below will be positive in this regard, i.e, will show that *if* a system obeys EPI on this level, and also the model of Sec. IV, then it obeys allometry.

In the next two sections we proceed to form the information functionals  $I(a)$  and  $J(a)$ , and then use them in the EPI principle (2).

## VI. DATA INFORMATION $I$

We first evaluate the information  $I(a)$ . The aim is to relate  $I(a)$  to the unknown system function  $f(x, a)$ , so that EPI principle (2) can be implemented through variation of  $f(x, a)$ .

From Eq. (1a), the average over  $y$  explicitly gives

$$I = I(a) = \int dy p(y|a) \left[ \frac{\partial}{\partial a} \ln p(y|a) \right]^2. \quad (6)$$

This takes the more specialized form (11), as shown next.

Since  $x$  is random, Eq. (5) actually represents the transformation of a random variable



$x$  to a random variable  $y$ . Therefore, elementary probability theory [30] may be used to connect the respective probability laws  $p_X(x)$  and  $p(y|a)$ , as

$$p(y|a)dy = p_X(x)dx, \quad dy > 0, \quad dx > 0. \quad (7)$$

We used  $p_X(x|a) = p_X(x)$  since, as previously discussed, a mass value  $x$  is selected independently of the choice of attribute. By (5),

$$\frac{dy}{dx} = C f'(x, a) \quad (8)$$

where the prime denotes  $\partial/\partial x$ . Combining Eqs. (7) and (8) gives

$$p(y|a) = \frac{p_X(x)}{C|f'(x, a)|}. \quad (9)$$

This is to be used in Eq. (6) to form  $I$ . First, taking a logarithm and differentiating gives

$$\frac{\partial}{\partial a} \ln p(y|a) = -\frac{\partial}{\partial a} \ln |f'(x, a)|. \quad (10)$$

Conveniently, both  $p_X(x)$  and the constants  $C$  have dropped out. Using the results (7) and (10) in Eq. (6) gives

$$I = \int dx \, p_X(x) \left[ \frac{\partial}{\partial a} \ln |f'(x, a)| \right]^2. \quad (11)$$

That is, the averaging  $\langle \rangle$  is now explicitly over the random variable  $x$ . Also,  $I$  is now related to the unknown function  $f(x, a)$ , as was required.

## VII. SOURCE INFORMATION $J(a)$

### A. Microlevel contributions

Recalling the model assumption (i) of Sec. IV,  $J(a)$  originates at the cell level. In general, some cells and cell groups contribute independently, and others dependently, to  $J(a)$ . Then, by the additivity property of Fisher information [4], the total information  $J(a)$  is simply *the signed sum of positive and negative* information contributions from the independent cells and cell groupings of the organism. A well-behaved function  $J(a)$  can of course be represented over a limited  $a$ -interval by a *Fourier series* of such terms. What interval size should be used?

Here we use model assumption (i) (Sec. IV) of a unit interval. A unit interval of  $a$ -space seems reasonable from various viewpoints. First, it is fundamental to many physical effects, such as in solid state physics where the number of degrees of freedom *per unit energy interval* is of fundamental importance. Second, a unit interval is certainly the *simplest* possible choice of an interval, and hence preferred on the basis of Occam's razor.

The alternative model assumption (v) (Sec. IV) of a *general* interval size  $\Delta a = L$  is taken up in Sec. X.

## B. Fourier analysis

In Sec. IV, item (i), the information  $J(a)$  was modeled as propagating waves. This can be substantiated. Heat or entropy propagates via plane wave-Fourier series [31],[32]. Fisher information  $J(a, t)$  is, like entropy, a measure of disorder, monotonically decreasing with an increase in time  $t$  [3],[4],[20]. Moreover, both the flux of heat/disorder [32] and the flow of information  $J(a, t)$  obey Fokker-Planck equations. We assume steady-state boundary conditions so that  $J(a, t) = J(a)$ . (The attributes supply information at a constant rate in time.) The general solution of this Fokker-Planck equation over a unit interval of  $a$  (as above) is a simple Fourier series [31],[32]

$$J(a) = \sum_{0 \leq a \leq 1} F_m \exp(2\pi i m a), \quad F_m = \int_0^1 da' J(a') \exp(-2\pi i m a') \quad (12a)$$

$$J(a) \geq 0, \quad i = \sqrt{-1}.$$

However, this series is inadequate for our purposes. First, Eqs. (3a,b) hold over an infinite range  $-\infty \leq a \leq \infty$  of attribute values, not only over a unit interval. Second, we expect function  $J(a)$  to be an even function,

$$J(a) = J(-a) \quad (12b)$$

since there is no reason to expect a negative attribute value to provide more information than its corresponding positive value. One way to accomplish the range  $-\infty \leq a \leq \infty$  is to form the Fourier series for  $J(a)$  over a *sequence* of symmetrically placed, half-unit interval pairs  $(-1/2 \leq a \leq 0)$  and  $(0 \leq a \leq 1/2)$ ;  $(-1 \leq a \leq -1/2)$  and  $(1/2 \leq a \leq 1)$ ; etc. These

are denoted as

$$a = \pm \left( \frac{j}{2}, \frac{j+1}{2} \right), \quad j = 0, 1, 2, \dots \quad (12c)$$

Each interval number  $j$  defines in this way a total *unit* interval for  $a$ , as required. The *half*-unit intervals (12c) are contiguous and span all of  $a$ -space. The  $J(a)$  for each interval obeys [31]

$$\begin{aligned} J(a)_{\pm(j/2, (j+1)/2)} &= \sum_m B_{mj} \exp(4\pi i m a), \quad J(a) \geq 0 \\ B_{mj} &= 2 \int_{j/2}^{(j+1)/2} da' J(a') \exp(-4\pi i m a'), \quad j = 0, 1, 2, \dots \end{aligned} \quad (12d)$$

Thus each value of  $j$  identifies an interval over which  $J(a)$  is defined by a distinct set of Fourier coefficients  $B_{mj}$ ,  $m = 1, 2, \dots$ . Since these intervals (12c) are contiguous and span  $a$ -space, the resulting  $J(a)$  is defined over all  $a$ -space as required. The factors 4 in the exponents, which will prove decisive, arise because each  $a'$ -integration (12d) is over an interval of length 1/2 (rather than 1 as in (12a)).

This simplifies further. Because each  $J(a)$  is an information and therefore *real*, (12d) becomes

$$J(a)_{\pm(j/2, (j+1)/2)} = \sum_m B_{mj}^{(re)} \cos(4\pi m a) - \sum_m B_{mj}^{(im)} \sin(4\pi m a), \quad j = 0, 1, 2, \dots \quad (12e)$$

where *(re)* and *(im)* denote real and imaginary parts.

Requirement (12b) of symmetry can only be obeyed if generally  $B_{mj}^{(im)} = 0$  for all  $m$ , so that

$$J(a)_{\pm(j/2, (j+1)/2)} = \sum_m A_{mj} \cos(4\pi m a), \quad A_{mj} \equiv B_{mj}^{(re)}, \quad j = 0, 1, 2, \dots \quad (12f)$$

Next, using  $B_{mj}^{(im)} = 0$  and that  $J(a')$  is real in the 2nd Eq. (12d) indicates that

$$B_{mj} = 2 \int_{j/2}^{(j+1)/2} da' J(a') \cos 4\pi m a' = B_{mj}^{(re)} \equiv A_{mj}, \quad j = 0, 1, 2, \dots \quad (12g)$$

By Eq. (2),  $J(a)$  must obey positivity [3],[4]. Therefore, the coefficients  $A_{mj}$  must be constrained to give positive or zero values  $J(a)$  at all  $a$ .

### VIII. PARTICULAR EPI PROBLEM

For generality of results, in the analysis that follows we will regard the cellular contributions  $A_{mj}$  in (12f) as arbitrary, except for causing symmetry (12b) and positivity (12d) in  $J(a)$ .

Using the particular informations (11) and (12f) in the general EPI principle (2) gives a problem

$$I - J = \int dx p_X(x) \left[ \frac{\partial}{\partial a} \ln |f'(x, a)| \right]^2 \quad (13)$$

$$- \int dx p_X(x) \sum_m A_{mj} \cos(4\pi m a) = \text{extremum}, \quad j = 0, 1, 2, \dots$$

Here a choice of  $a$  defines 1:1 a choice of interval  $j$ , via Eq. (12c), and therefore a choice of coefficients  $A_{mj}$ ,  $m = 1, 2, \dots$ . For mathematical convenience, we appended a multiplier of 1 (a normalization integral  $\int dx p_X(x)$ ) to the second sum  $J$ .

As discussed in Sec. V A, we seek the channel functions  $f(x, a)$  and (in biological cases) the system parameters  $a$  that extremize (13), in the presence of any *fixed* source PDF  $p_X(x)$ . Accordingly, the extremum in the principle (13) is first attained through variation of functions  $f(x, a)$  and then, in biological cases, through the additional variation of parameters  $a$ . The mass PDF  $p_X(x)$  is *not* varied, and turns out to not affect the answer. Thus, *the channel is optimized in the presence of a given source*.

#### A. Synopsis of the approach

The basic approach consists of three overall steps, as carried through in Sec. VIII B - Sec. IX E:

(1) The information flow  $I - J$  is extremized through choice of system function  $f(x, a)$ , in the presence of any fixed PDF mass law  $p_X(x)$ . This gives a general power law for its derivative  $\partial f(x, a)/\partial x \equiv f'(x, a)$ ,

$$f'(x, a) = h(x)^{a-1}, \quad a \text{ real.} \quad (14a)$$

[Eq. (20)]. Quantity  $h(x)$  is some unknown base function of  $x$ .

(2) The base function  $h(x)$  is found, by further extremizing  $I - J$  with respect to it, giving  $h(x) = b_1 x$  [Eq. (38)]. Using this in (14a) gives

$$f(x, a) = x^a \quad (14b)$$

[Eq. (42)] after an integration. An irrelevant constant is ignored. By Eq. (5), this achieves derivation of the general allometric law (3a).

(3) Finally, for a system that is biological,  $I - J$  is extremized with respect to the choice of  $a$ , which gives  $a = n/4$  [Eq. (25)]. Using this in (14b) gives

$$f(x, a) = x^{n/4}. \quad (14c)$$

This is the biological allometric law (3b). The approach (1)-(3) is now carried through.

### B. Primary variation of the system function leads to a family of power-laws

The aim is to find the channel function  $f(x, a)$  in the presence of a fixed source function  $p_X(x)$ . Hence we first vary  $f(x, a)$ , by use of the calculus of variations, holding the function  $p_X(x)$  constant. Conveniently, it will drop out during the variation. The Lagrangian for the problem is, by definition, the integrand of (13)

$$\mathcal{L} = p_X(x) \left[ \frac{\partial}{\partial a} \ln g(x, a) \right]^2 - p_X(x) \sum_m A_{mj} \cos(4\pi m a), \quad j = 0, 1, 2, \dots \quad (15a)$$

where we introduced a new function  $g$  defined as

$$|f'(x, a)| \equiv g(x, a). \quad (15b)$$

In this way the function  $g(x, a)$  replaces  $f(x, a)$  as the quantity to vary in (15a). Keeping in mind that the PDF  $p_X(x)$  on mass remains a *fixed* function during the variation, the Lagrangian (15a) is readily differentiated as

$$\frac{\partial \mathcal{L}}{\partial(\partial g / \partial a)} = 2 p_X(x) \frac{\partial g / \partial a}{g^2} \quad \text{and} \quad \frac{\partial \mathcal{L}}{\partial g} = -2 p_X(x) \frac{(\partial g / \partial a)^2}{g^3}, \quad g \equiv g(x, a). \quad (16)$$

Using these in the Euler-Lagrange equation [31]

$$\frac{\partial}{\partial a} \left( \frac{\partial \mathcal{L}}{\partial(\partial g / \partial a)} \right) = \frac{\partial \mathcal{L}}{\partial g} \quad (17)$$

gives, after some trivial cancellation,

$$\frac{\partial}{\partial a} \left[ \frac{\partial g / \partial a}{g^2} \right] = - \frac{(\partial g / \partial a)^2}{g^3}, \quad g \equiv g(x, a). \quad (18)$$

Thus, the unknown PDF  $p_X(x)$  has dropped out, as we anticipated above. Doing the indicated differentiation gives after some algebra

$$g \frac{\partial^2 g}{\partial a^2} - \left( \frac{\partial g}{\partial a} \right)^2 = 0. \quad (19)$$

The general solution to this can be found by using  $g \equiv \exp(k)$ ,  $k \equiv k(x, a)$ , in (19) and solving the resulting differential equation for  $k$ . The answer is  $k = K(x)a + L(x)$ , with  $K(x), L(x)$  arbitrary functions. Exponentiating back to  $g$  gives an answer

$$g(x, a) = h(x)^{a-1}, \quad (20)$$

where  $h(x) \equiv \exp(K(x))$  is an arbitrary real function of  $x$  called the "base function," and we took  $L(x) \equiv -K(x)$ . The latter choice gives the term  $-1$  in the exponent of (20), for later numbering of the attributes (see also (v), Sec. IV). The solution (20) may be readily shown to satisfy differential equation (19), keeping in mind that its derivatives are with respect to  $a$  and not  $x$ .

Hence the solution to the problem has the general form of a *power law*. That is, on the basis of optimal information flow  $J \rightarrow I$ , nature generally acts to form power-law solutions for the rate of change  $g(x, a)$  of the channel function.

The general solution (20) contains a general base function  $h(x)$  of the mass. This function will be found in Sec. IX. Also, the values of the power  $(a - 1)$  of  $h(x)$  to be used for the biological laws are not yet fixed. These unknown powers will next be fixed, as the 2nd optimization step.

### C. Variation of the attribute parameters gives powers $\mathbf{a} \equiv \mathbf{a}_n = \mathbf{n}/4$

Here, by premise (iii) of Sec. IV, we vary  $a$ , for use in the biological laws. (Note that this will not affect the general law (3a) derivation since  $a$  so obtained [Eq. (25)] will *not* be used in that derivation.) Since  $a$  is a discrete variable, ordinary calculus is used, differentiating  $\partial/\partial a$  Eq. (13) and equating the result to zero. This gives, after use of (15b),

$$\begin{aligned}
& \frac{\partial}{\partial a} \int dx p_X(x) \left[ \frac{\partial g(x, a)/\partial a}{g(x, a)} \right]^2 \\
& - \frac{\partial}{\partial a} \left[ \int dx p_X(x) \sum_m A_{mj} \cos(4\pi m a) \right] \\
& = 0, \quad j = 0, 1, 2, \dots
\end{aligned} \tag{21}$$

The first derivative term in (21) is next shown to be zero. Its derivative  $\partial/\partial a$  operation may be moved to within the integrand, giving

$$\frac{\partial}{\partial a} \left( \frac{g_a}{g} \right)^2, \quad g_a \equiv \frac{\partial g(x, a)}{\partial a}. \tag{22}$$

Carrying out the indicated derivative  $\partial/\partial a$  gives

$$2 \left( \frac{g_a}{g} \right) \frac{\partial}{\partial a} \left( \frac{g_a}{g} \right) = 2 \left( \frac{g_a}{g} \right) \left( \frac{g g_{aa} - g_a^2}{g^2} \right) = 0 \tag{23}$$

by Eq. (19). Eq. (19) could be used since the biological optimization requires the *simultaneous* satisfaction of both conditions (17) and (21).

We showed in the preceding paragraph that the the left-hand term in (21) becomes zero after the indicated differentiation, that is,  $\partial I/\partial a = 0$ . This has two important consequences. First, as will be shown below,  $I$  then does not depend upon  $a$  for the power law solution (20).

Second, only the right-hand term of (21) now remains. It defines a problem

$$\begin{aligned}
& \frac{\partial}{\partial a} \left[ p_X(x) \sum_m A_{mj} \cos(4\pi m a) \right] \\
& = -p_X(x) \sum_m A_{mj} (4\pi m) \sin(4\pi m a) = 0, \quad j = 0, 1, 2, \dots
\end{aligned} \tag{24}$$

(Note that  $\partial \cos(4\pi m a)/\partial a = -4\pi m \sin(4\pi m a)$  within any interval  $j$ .) For arbitrary coefficients  $A_{mj}$ , the required zero is obtained if and only if

$$a \equiv a_n = \frac{n}{4}, \quad n = 0, \pm 1, \pm 2, \pm 3, \dots \tag{25}$$

since then the sine function in (24) becomes  $\sin(mn\pi) = 0$  for all integers  $m, n$ . Note that the solution values (25) form *in sequence* for the different unit intervals  $j$  given by (12c).

As examples: The interval for  $j = 0$  is  $(-1/2, 0)$ ,  $(0, 1/2)$  and contains solution values (25)  $a = 0, \pm 1/4, \pm 2/4$ . The interval for  $j = 1$  is  $(-1, -1/2)$ ,  $(1/2, 1)$  and contains solutions  $a = \pm 2/4, \pm 3/4, \pm 4/4$ . And so on, thereby forming *all* solutions (25).

Result (25) shows that the attribute value  $a$  must be a multiple of  $1/4$ , or, *the powers in the power law (20) are multiples of  $1/4$* . This is an important milestone in the biological derivation. We emphasize that it only could follow because of the *discrete* nature of the sum over  $m$ , which follows from the model assumption (i) (Sec. IV) that information originates on the level of the discrete cells.

## IX. SECONDARY EXTREMIZATION THRU CHOICE OF $h(x)$

The solution (20) to the extremization problem (13) of  $I - J = \text{extrem.}$  was found to contain an arbitrary function  $h(x)$ . Clearly the appropriate  $h(x)$  is the one that further extremizes  $I - J$ . We seek this function here. First we establish a general property of  $h(x)$ .

### A. Special form of function $h(x)$

Here we show that  $h(x)$  can be expressed as a linear term in  $x$  plus a function that is at least quadratic in  $x$ . Function  $h(x)$  can be generally expanded in Taylor series as

$$h(x) = b_0 + b_1x + b_2x^2 + b_3x^3 + \dots \quad (26)$$

Differentiating (5), then using (26) in (15b) and (20) gives, in sequence,

$$\begin{aligned} \frac{dy_{nk}}{dx} &= C_{nk} \frac{df(x, a_n)}{dx} = C_{nk} g(x, a_n) = C_{nk} h(x)^{a_n-1} \\ &= C_{nk} (b_0 + b_1x + b_2x^2 + \dots)^{a_n-1}. \end{aligned} \quad (27)$$

Then

$$\lim_{x \rightarrow 0} \frac{dy_{nk}}{dx} = C_{nk} b_0^{a_n-1} \equiv \frac{C_{nk}}{b_0^{1-a_n}}. \quad (28)$$

We now use the model properties (4a), (4b). If  $a_n < 1$  then limit (4a) holds. This can only be obeyed by (28) if

$$b_0 = 0. \quad (29)$$



Consequently, by (26)  $h(x) = b_1x + b_2x^2 + b_3x^3 + \dots$  or

$$h(x) = b_1x + [k(x)]^2, \quad k(x) \equiv x\sqrt{b_2 + b_3x + \dots} \quad (30)$$

for some function  $k(x)$ . By the square root operation in (30), the latter is in general either pure real or pure imaginary at each  $x$ ; it is found next.

### B. Resulting variational principle in base function $h(x)$

Using definition (15b), and Eq. (20) in Eq. (11), gives an information level

$$\begin{aligned} I &= \left\langle \left[ \frac{\partial}{\partial a} \ln (h(x)^{a-1}) \right]^2 \right\rangle = \left\langle \left[ \frac{\partial}{\partial a} (a-1) \ln h(x) \right]^2 \right\rangle \\ &= \langle \ln^2 h(x) \rangle \end{aligned} \quad (31)$$

after obvious algebra. Quantity  $a$  has dropped out.

The information difference  $I - J$  is to be extremized in a *total sense*. The base function  $h(x)$  that defines  $I$  in (31) has been expressed in terms of a new function  $k(x)$  [Eq. (30)]. Hence  $I - J$  must be further (secondarily) extremized *through variation of function  $k(x)$* . Using EPI result (30) in (31), and combining this with (12f) and (25), gives a new problem

$$I - J = \langle \ln^2 [b_1x + k^2(x)] \rangle - \sum_m A_{mj} (-1)^{mn} \equiv \text{extremum} \quad (32)$$

in  $k(x)$ .

### C. Secondary variational principle in associated function $k(x)$

Since the  $A_m$  are independent of  $k(x)$ , the net Lagrangian in (32) for varying  $k(x)$  is

$$\mathcal{L} = p_X(x) \ln^2 [b_1x + k^2(x)] . \quad (33)$$

Function  $p_X(x)$  arises out of the expectation operation  $\langle \rangle$  in (32), and is also independent of  $k(x)$ . The general Euler-Lagrange equation for problem (33) is [31]

$$\frac{d}{dx} \left( \frac{\partial \mathcal{L}}{\partial k'(x)} \right) = \frac{\partial \mathcal{L}}{\partial k(x)}, \quad k'(x) \equiv dk/dx. \quad (34)$$

Since  $\mathcal{L}$  in (33) does not depend upon  $k'(x)$ , the left-hand side of (34) is zero. Also,

differentiating (33) gives

$$\frac{\partial \mathcal{L}}{\partial k(x)} = \frac{2 p_X(x) \ln [b_1 x + k^2(x)]}{b_1 x + k^2(x)} 2k(x) \equiv 0. \quad (35)$$

Once again,  $p_X(x)$  is merely a constant multiplier, dropping out of the problem. Eq. (35) has two formal solutions.

#### D. Result $k(x) = 0$ , giving base function $h(x)$ proportional to $x$

The first formal solution to (35) is

$$b_1 x + k^2(x) \equiv h(x) = 1, \quad (36)$$

the middle identity by (30). The second solution is

$$k(x) = 0. \quad (37)$$

(Notice that this holds regardless of whether  $k(x)$  is pure real or pure imaginary.)

However, one solution is readily eliminated. The candidate (36) when used in (31) gives  $I = \langle [\ln 1]^2 \rangle = 0$ . This extremum is the *absolute minimum* value possible for Fisher information. However,  $I = 0$  is rejected since then the observed value  $y$  of the attribute would unrealistically provide no information about the attribute. Hence the solution (36) is rejected.

By comparison, the candidate (37) when used in (30) gives

$$h(x) = b_1 x, \quad (38)$$

and consequently

$$I \equiv I_{\text{extrem}} = \langle [\ln(b_1 x)]^2 \rangle. \quad (39)$$

by (31). Information (39) is generally nonzero, thereby representing a subsidiary minimum, which makes sense on the grounds that the observation must contain at least some information. Hence the solution (37), (38) is accepted.

#### E. Final allometric laws

We are now in a position to form the final allometric laws (3a,b) for, respectively, general and living systems. Substituting the solution (38) into Eqs. (15b) and (20) gives  $|f'(x, a)| =$

$(b_1x)^{a-1}$  or

$$f'(x, a) = \pm(b_1x)^{a-1}. \quad (40)$$

Indefinitely integrating gives

$$f(x, a) = \pm b_1^{a-1} \int dx x^{a-1} \equiv \pm a \int dx x^{a-1}, \quad (41)$$

for a suitably defined  $b_1$ . An additive constant in (41) is taken to be zero by asymptotic prior knowledge (4b): In all attribute parameter cases  $a > 1$ , as  $x \rightarrow 0$  it is required that the attribute value  $y_{nk} \rightarrow 0$ , and hence by Eq. (5) likewise  $f(x, a) \rightarrow 0$ . The integral (41) is directly evaluated as

$$f(x, a) = x^a. \quad (42)$$

We used the fact that the attribute values  $y$  are positive [Eqs. (3a,b)] in order to rule out the negative alternative.

The *general* allometric law (3a) is to hold for a priori empirically defined powers  $a_n$  (see (iii), Sec. IV). Here the specific powers (25) that held for optimization of  $I - J$  do not apply. The solution is more simply the combination of Eqs. (42) and (5). Reinserting subscripts gives

$$y_{nk} \equiv C_{nk} f(x, a_n) = Y_{nk} x^{a_n}, \quad \text{so that} \quad Y_{nk} \equiv C_{nk}, \quad n = 0, \pm 1, \pm 2, \dots \quad (43)$$

This confirms the general allometric law (3a) for empirically known  $a_n$ .

Next we turn to the *biological* allometric law, which is modelled ( (iii), Sec. IV) to hold for the particular powers  $a_n$  given by (25) that enforce a further extremization in the problem (2). Using powers (25) in the power law solution (42), and also using (5), gives

$$y_{nk} \equiv C_{nk} f(x, a_n) = Y_{nk} x^{n/4}, \quad \text{so that} \quad Y_{nk} \equiv C_{nk}, \quad n = 0, \pm 1, \pm 2, \dots \quad (44)$$

This is the law (3b). As contrasted with laws (43), the powers  $a_n$  are here purely multiples of  $1/4$ .

## X. ALTERNATIVE MODEL $\Delta a = L$

The preceding derivation assumed a priori a unit fundamental length  $\Delta a = 1$  ((i), Sec. IV). A stronger derivation would allow  $\Delta a = L$  with  $L$  general. With  $\Delta a = L$ , the half-unit interval pairs in Sec. VII B are replaced with pairs of length  $L/2$ . Also, Eqs. (12c)-(12g) now hold [31] under the replacements  $j \rightarrow jL$ ,  $(j+1) \rightarrow (j+1)L$ , and  $m \rightarrow m/L$ . Consequently the requirement of zero for Eq. (24) now becomes one of zero for  $\sin(4\pi ma/L)$ . The solution is  $a \equiv a_n = nL/4$ . Hence, by (43) the biological power law is now  $y_{nk} = Y_{nk}x^{nL/4}$  instead of (44). Also, now  $a_1 = 1 \cdot L/4 = L/4$ . But by model assumption (v) of Sec. IV,  $a_1 \equiv 1/4$ . It results that  $L = 1$ . Consequently the quarter-power law (44) results once again.

## XI. SUMMARY

After introducing Fisher data information  $I$  in Sec. I, the information is used in the EPI principle (2) of Sec. II. The general allometric laws of science are discussed in Sec. III A, a subset from biology is discussed in Sec. III B, and past explanations of biological allometry are discussed in Sec. III C. The limited scope of the EPI derivation is discussed in Sec. III C. The prior knowledge assumed in the EPI derivation is given in Sec. IV. This includes the assumption that the source information  $J$  originates at the level of discrete cells, and propagates from there into measurement space. Also used is specific limiting behavior of the allometric laws near the origin. Caveats to the approach are discussed in Sec. V B and below in Sec. XII. The rest of the paper is concerned with deriving the allometric laws from these assumptions. The derivation concurrently applies to both inanimate and biological cases. A brief synopsis of the mathematics of the approach is given in Sec. VIII A.

The detailed approach is given in Secs. VIIIB - IX E, with an alternative aspect addressed in Sec. X.

## XII. DISCUSSION

This paper has the limited aim (3c) of *establishing necessity* for allometry. It shows that if a system obeys the model of Sec. IV and also obeys EPI through variation of its channel function  $f(x, a)$ , it must obey allometry. However, this does not necessarily imply the converse – that any system that obeys allometry must also obey EPI and the model.

(Note that this in fact might be true, but is regarded as outside the scope of the paper.) Also, *not all* systems obey allometry. Then, by the necessity (3c) proven in this paper, such systems do not obey the model of Sec. IV and/or EPI.

By the overall approach, the allometric laws (3a,b) follow as the effect of a flow of information  $J \rightarrow I$  from an attribute source to an observer. We saw that the derivation for general laws (3a) slightly differs from that for biological laws (3b). Each general law (3a) accomplishes an extremization of the loss of information  $I - J$  through variation of the system function  $f(x, a_n)$  and its subfunctions  $h(x)$  and  $k(x)$ . By comparison, the biological allometric laws (3b) accomplish the extremization with respect to both these functions *and* the system parameters  $a_n$ . The extra optimization with respect to the  $a_n$  reflects the specialized nature of biological allometry. But, why should biological systems be so specialized?

The answer is that, as compared to nonliving systems, biological systems have resulted from Darwinian *evolution*. Thus, evolution is postulated ((iii), Sec. IV) as selecting particular attribute parameters  $a_n$  that optimize the information flow loss  $I - J$ . The postulate is reasonable. Survival and proliferation within an adaptive landscape favors optimization of phenotypic traits which, in turn, confers maximal fitness on the individual. Here the phenotype traits are, in fact, the attribute parameters  $a_n$ . Therefore, the  $a_n$  will evolve into those values that favor maximal fitness. Meanwhile, maximal fitness has been shown [4], [23] to result from optimal information flow loss  $I - J = \textit{extrem}$ . (The latter gives rise to the Lotka-Volterra equations of growth which, in turn, imply maximal fitness through "Fisher's theorem of genetic change.") Therefore, it is reasonable that the same parameter values  $a_n$  that satisfy evolution will also satisfy  $I - J = \textit{extrem}$ .

In a related derivation [24], under the premise that *in situ* cancer is likewise in an evolutionary extremized state – now of transmitting *minimal* information about its age and size – the EPI output result is the correct law of cancer growth, again a power law form (3a). However, here  $x$  is the time and  $a_n = 1.618\dots$  is the Fibonacci golden mean. Also, as here, the information is optimized with respect to the exponent  $a_n$ . This is also further evidence that the premise ((iii), Sec. IV) of evolutionary efficiency is correct.

It was assumed as prior knowledge ((iv), Sec. IV) that in biological cases (3b) the independent variable  $x$  is the *mass* of the organism. That is, laws (3b) are scaling laws covering a range of sizes, where the sizes are specified uniquely by mass values  $x$ . Aside from being a postulate of the derivation, this is reasonable on evolutionary grounds. By

its nature, the process of evolution favors systems that are close to being *optimized* with respect to the energy [and information] they distribute [9] to phenotypic traits at its various scales. On this basis only a dependence upon absolute size or mass would remain.

The precise form of the biological function  $J(a)$  is unknown. It is possible that it is periodic, repeating itself over each fundamental interval  $j$ . This implies that all  $A_{mj} = A_m$ ,  $m = 1, 2, \dots$  irrespective of  $j$ . Interestingly, for such periodicity  $J(a)$  breaks naturally into 2 classes. Back substituting any one coefficient (25) into the Fourier representation (12f) now gives

$$J(a_n) = J(n/4) = \sum_m A_m \cos(mn\pi) = \sum_m A_m (-1)^{mn}. \quad (45)$$

Since the  $A_m$  remain *arbitrary*, this still represents an arbitrary information quantity  $J(a_n)$  for  $n = 0$  or  $1$ . However, for higher values of  $n$  the form (45) repeats, giving

$$J(\pm a_3) = J(\pm a_5) = \dots = J(\pm a_1), \quad (46a)$$

and

$$J(\pm a_2) = J(\pm a_4) = \dots = J(\pm a_0). \quad (46b)$$

Hence the odd numbered attributes  $n = \pm 1, \pm 3, \pm 5, \dots$  all share one fixed level of ground truth information  $J$  about their values  $a_n$ , and the even numbered attributes  $n = 0, \pm 2, \pm 4, \pm 6, \dots$  share another. Consequently, the source information of the channel is specified by but *two* independent values, (say)  $J(a_0)$  and  $J(a_1)$ . Or, the allometric relations result from two basic sources of information. As we found, the numerical values of the two information levels remain arbitrary, since the coefficients  $A_m$  are arbitrary.

Finally, it is worthwhile considering why *biologically* there should be but two classes of information. The postulate (i) of Sec. IV that discrete cells are the sources of information enters in once again. This ultimately gave rise to the sum (12f) representing the source information  $J(a)$  for the attribute. The sum is over the biological cells and, by Eqs. (46a,b) there are only two independent information sources. On this basis each cell must provide *two* independent sources of attribute information. The existence of two such sources is, in fact, consistent with recent work [33] which concludes that *cellular DNA* and *cellular transmembrane ion gradients* are the sources.

## Acknowledgments

We thank Prof. Daniel Stein of the Courant Inst., N.Y.U., for checking the math and making valuable suggestions on the modeling. Prof. Patrick McQuire of the Center for Astrobiology (CSIC/INTA), Madrid, provided valuable comments on biological aspects of the manuscript. Finally, valuable support was provided by H. Cabezas of the Sustainable Technologies Division, Environmental Protection Agency.

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